Granzyme B (nM)

DNA-PK

0.12 1.25 12.5 Granzyme B (nM)

NuMA

1.25 12.5 50 Granzyme B (nM)

Caspase-7

-12

Granzyme B (nM) 1.25 12.5 50

Caspase-3

Granzyme B (nM)

PARP

-3414 Act 1014-3:360 2 ROBOW

F16. 2 Caspase-3 PARP Granzyme B No protease Caspase-3 6 NUMA Granzyme B No protease (anti-N-terminal Ab) Caspase-3 **DNA-PKcs** Granzyme B No protease ş (anti-C-terminal Ab) Caspase-3 **DNA-PKcs** B emyznsið No protease

F16.3

SP1

If the little with the little with the with the

No additions

Caspase-3

Caspase-4

Caspase-4

Caspase-4

Caspase-4

Caspase-4

Caspase-4

Caspase-

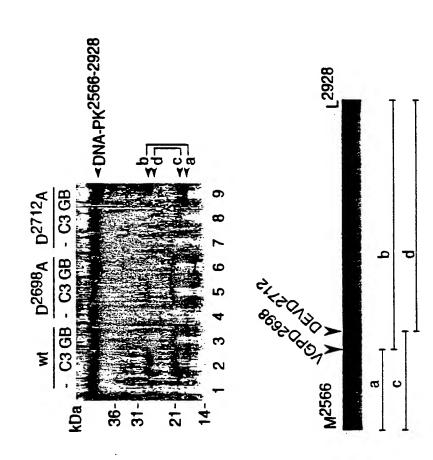
2

3

1

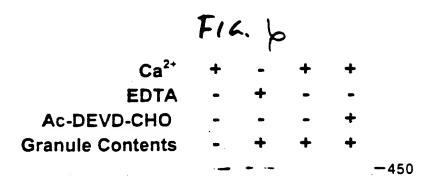
F16. 4

F16.5

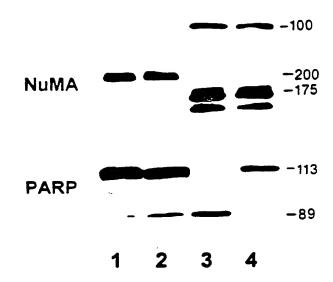


Figures Service sources Significant Signif

H"H H"H mild H"H has hear hear had had had had had been been as a second of the hear had hear hear



DNA-PKcs



F16. 7

LAK + - + + K562 - + + + DEVD - - - +

__ _ _ _ _ _ intact

DNA-PK_{cs}

__150kDa

→ −100kDa

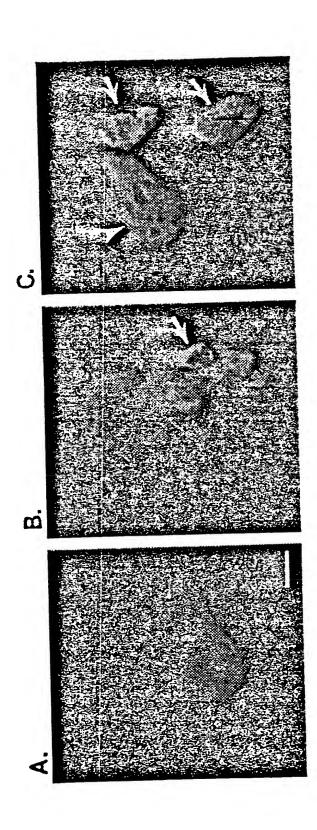
PARP

- intact

- 89kDa

1 2 3 4

FIGURE 8



Protein

FIG. 9A

LOCUS 284337 12-APR-1996 2101 aa DEFINITION NuMA protein - human. ACCESSION 284337 g284337 PID DBSOURCE PIR: locus A42184 summary: #length 2101 #molecular-weight 236296 #checksum 8715. PIR dates: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Apr-1996. KEYWORDS SOURCE human. ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; REFERENCE 1 (residues 1 to 2101) AUTHORS Compton, D.A., Szilak, I. and Cleveland, D.W. Primary structure of NuMA, an intranuclear protein that defines a novel pathway for segregation of proteins at mitosis JOURNAL J. Cell Biol. 116 (6), 1395-1408 (1992) MEDLINE 92176238 REFERENCE 2 (residues 1 to 2101)
AUTHORS Tang, T.K., Tang, C.J., Chen, Y.L. and Wu, C.W. Nuclear proteins of the bovine esophageal epithelium. II. The NuMA gene gives rise to multiple mRNAs and gene products reactive with monoclonal antibody W1 JOURNAL J. Cell. Sci. 104 (Pt 2), 249-260 (1993) MEDLINE 93280231 REFERENCE 3 (residues 1 to 2101) AUTHORS Harborth, J., Weber, K. and Osborn, M. Epitope mapping and direct visualization of the parallel, in-register arrangement of the double-stranded coiled-coil in the NuMA protein **JOURNAL** EMBO J. 14 (11), 2447-2460 (1995) MEDLINE 95300777 **FEATURES** Location/Qualifiers source 1..2101

> /organism="Homo sapiens" /db_xref="taxon:9606"

/product="NuMA protein"

1..2101

FIG. 9B

1	mtlhatrgaa	llswvnslhv	adpveavlql	gdcsifikii	drihgteegq	gilkapvser
61	ldfvcsflqk	nrkhpsspec	lvsagkvleg	selelakmtm	lllyhstmss	ksprdwegfe
121	ykiqaelavi	lkfvldhedg	lnlnedlenf	lgkapvpstc	sstfpeelsp	pshqakreir
181	flelgkvass	ssgnnflsgs	paspmgdilq	tpqfqmrrlk	kqladersnr	delelelaen
241	rklltekdaq	iammqqridr	lallnekgaa	splepkelee	lrdknesltm	rlhetlkqcq
301	dlkteksqmd	rkinglseen	gdlsfklref	ashlqqlqda	lnelteehsk	atgewlekga
	qlekelsaal					
421	eaatlaannt	qlqarvemle	tergqqeakl	laerghfeee	kqqlsslitd	lassisnlsq
481	akeeleqasq	ahgarltaqv	asltselttl	natigggdge	laglkqqake	kqaqlaqtlq
541	qqeqasqglr	hqveqlsssl	kqkeqqlkev	aekgeatrqd	hagglataae	ereaslrerd
601	aalkqleale	kekaakleil	ggglgvanea	rdsagtsvtg	agrekaelsr	kveelgacve
661	tarqeqheaq	aqvaelelql	rseggkatek	ervagekdgl	qeqlqalkes	lkvtkgslee
	ekrraadale					
781	etevlrrela	eamaaghtae	seceglvkev	aawrdgyeds	qqeeaqygam	fqeqlmtlke
841	ecekarqelq	eakekvagie	shselqisrq	qnklaelhan	laralqqvqe	kevragklad
	dlstlqekma					
961	cstqaalqam	ereaeqmgne	lerlraalme	sągąągeerg	qqerevarlt	qergraqadl
	alekaarael					
1081		keqlakkeke				
1141		eaerasraer				
1201	dhskaedewk	aqvargrqea	erknslissl	eeevsilnrq	vlekegeske	lkrlvmaese
	ksqkleesca					lrqeltsqae
1321	raeelgqelk	awqekffqke	qalstlqleh	tstqalvsel	lpakhlcqql	qaeqaaaekr
	hreeleqskq					asyaeqlsml
	kkahgllaee					laevqreaqs
1501	tarelevmta	kyegakvkvl	eerqrfqeer	gkltagveel	skkladsdga	skvqqqklka
1561	vqaqggesqq					
1621	lrsleqlqke	nkelraeaer			hltaqvrsle	
1681	rdlgkfqvat		kpqldlsids		lsitsklprt	qpdgtsvpge
1741		pkveslesly				
1801		veepdsanss				ygnsallslp
1861		rrsqagvssg				
1921		slslgtitde				
1981		katscfprpm				
2041		rrgaskkals	kaspntrsgt	rrspriattt	asaataaaig	atprakgkak
2101	h					

FIG. 10A

LOCUS 107227 2115 aa10-NOV-1995 DEFINITION NuMA protein - human. ACCESSION 107227 PID g107227 DBSOURCE PIR: locus S23647 summary: #length 2115 #molecular-weight 238273 #checksum 4391. PIR dates: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995. **KEYWORDS** SOURCEhuman. ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; REFERENCE 1 (residues 1 to 2115)
AUTHORS Yang, C.H., Lambie, E.J. and Snyder, M. NuMA: an unusually long coiled-coil related protein in the mammalian nucleus JOURNAL J. Cell Biol. 116 (6), 1303-1317 (1992) MEDLINE 92176231 FEATURES Location/Qualifiers source 1..2115 /organism="Homo sapiens" /db_xref="taxon:9606" Protein 1..2115 /product="NuMA protein"

FIG. 10B

		•				
61 121 1241 1241 1361 1481 1661 1781 1181 1181 1181 1181 1181 11	qlekelsaal eaatlaannt akeeleqasq qqeqasqglr aalkqleale tarqeqheaq ekrraadale etevlrrela ecekarqelq dlstlqekma cstqaalqam alekaarael eelrqtvkql eqadslersl dhskaedewk ksqkleerlr raeelgqelk hreeleqskq kkahgllaee tarelevmta sdqaskvqqq ydakkqqnqe rsleaqvaha lprtqpdgts grktrsarrr	nrkhpsspec lkfvldhedg ssgnnflsgs iammqqridr rkinqlseen qdkkcleekn qlqarvemle ahgarltaqv hqveqlsssl kekaakleil aqvaelelql eqqrciselk eamaaqhtae eakekvagie atskevarle ereaeqmgne emrlqnalne keqlakkeke eaerasraer aqvargrqea llqaetasns awqekffqke aagglraell nrglgeranl kyegakvkvl klkavqaqgg lqeqlrsleq dqqlrdlgkf vpgepaspis ttqiinitmt lslpgyrptt	lvsaqkvleg lnlnedlenf paspmgdilq lallnekqaa gdlsfklref eilqgklsql tergqqeakl asltselttl kqkeqqlkev qqqlqvanea rseqqkatek aetrslveqh seceqlvkev shselqisrq tlvrkageqq lerlraalme qrvefatlqe hasgsgaqse dsaletlqgq erknslissl araaerssal qalstlqleh raqrelgeli grqfleveld eerqrfqeer esqqeaqrlq lqkenkelra qvatdalksr qrlppkvesl kkldveepds rssarrsqag	selelakmtm lqkapvpstc tpqfqmrrlk splepkelee ashlqqlqda eehlsqlqdn laerghfeee natiqqqdqe aekqeatrqd rdsaqtsvtq ervaqekdql krerkeleee aawreryeds qnelaelhan etasrelvke sqgqqqeerg alahalteke aagrteptgp leekaqelgh eeevsilnrq reevqslree tstqalvsel plrqkvaeqe qarekyvqel qkltaqveql aqlnelqaql eaerlghelq epqakpqldl eslyftpipa anssfystrs vssgappgrn	lllyhstmss sstfpeelsp kqladersnr lrdknesltm lnelteehsk ppqekgevlg kqqlsslitd laglkqqake haqqlataae aqrekaelsr qeelqalkes ragrkglear qqeeaqygam laralqqvqe paragdrqpe qqerevarlt gkdqelaklr klealraevs sqsalasaqr vlekegeske aekqrvasen lpakhlcqql rtaqqlraek aavradaetr evfqreqtkq sqkeqaaehy qaglktkeae sidsldlsce rsqaplessl apasqaslra sfymgtcqde	ksprdweqfe pshqakreir delelelaen rlhetlkqcq atqewlekqa dvlqletlkq lqssisnlsq kqaqlaqtlq ereaslrerd kveelqacve lkvtkgslee lqqlgeahqa fqeqlmtlke kevraqklad wleeqqgrqf qergraqadl gleaaqikel kleqqcqkqq elaafrtkvq lkrlvmaese lrqeltsqae qaeqaaaekr asyaeqlsml laevqreaqs veelskklad klqmekakth qtcrhltaqv egtplsitsk dslgdvfqds tsstqslarl peqlddwnri
1741 1801 1861	lprtqpdgts grktrsarrr gspdygnsal	vpgepaspis ttqiinitmt lslpgyrptt	qrlppkvesl kkldveepds rssarrsqag	eslyftpipa anssfystrs vssgappgrn	rsqaplessl apasqaslra sfymgtcqde	dslgdvfqds tsstqslarl peqlddwnri
1921 1981 2041 2101	ittrqqrkrv qadrrqsmaf	slephqgpgt silntpkklg	esrpsisigt peskkatscf nsllrrgask	prpmtprdrh	egrkqsttea	qkkaapastk

FIG. 11A

LOCUS 1362789 4096 aa 06-SEP-1996
DEFINITION DNA-activated protein kinase catalytic subunit - humi

DEFINITION DNA-activated protein kinase, catalytic subunit - human.

ACCESSION 1362789

PID g1362789

DBSOURCE PIR: locus A57099

summary: #length 4096 #molecular-weight 465420 #checksum 1795.

genetic: #gene GDB:PRKDC ##cross-references GDB:234702

#map_position 8q11.

PIR dates: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change

06-Sep-1996.

KEYWORDS DNA binding; DNA recombination; DNA repair; nucleus; phosphotransferase.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 4096)

AUTHORS Sipley, J.D., Menninger, J.C., Hartley, K.O., Ward, D.C., Jackson, S.P. and Anderson, C.W.

TITLE Gene for the catalytic subunit of the human DNA-activated protein kinase maps to the site of the XRCC7 gene on chromosome 8

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92 (16), 7515-7519 (1995)

MEDLINE 95365397

REFERENCE 2 (residues 1 to 4096)

AUTHORS Hartley, K.O., Gell, D., Smith, G.C., Zhang, H., Divecha, N., Connelly, M.A., Admon, A., Lees-Miller, S.P., Anderson, C.W. and Jackson, S.P.

TITLE DNA-dependent protein kinase catalytic subunit: a relative of phosphatidylinositol 3-kinase and the ataxia telangiectasia gene product

JOURNAL Cell 82 (5), 849-856 (1995)

MEDLINE 95401275

FEATURES Location/Qualifiers

source 1..4096

/organism="Homo sapiens"

/db_xref="taxon:9606"

Protein

1..4096

/note="DNA-PK-cs"

/product="DNA-activated protein kinase, catalytic subunit"

8 11 B...II smith

m

FIG. 11B

1 magsgagvrc sllrigetis aadrcgaala ghqlirgigq ecvissspav lalqtslvfs 61 rdfgllvfvr kslnsiefre creeilkflc iflekmgqki apysveiknt ctsvytkdra 121 akckipaldl likllqtfrs srlmdefkig elfskfygel alkkkipdtv lekvyellgl 181 lgevhpsemi nnaenlfraf lgelktqmts avrepklpvl agclkglssl lcnftksmee 241 dpqtsreifn fvlkairpqi dlkryavpsa glrlfalhas qfstclldny vslfevlikw 301 cahtnvelkk aalsalesfl kqvsnmvakn aemhknklqy emeqfygiir nvdsnnkels 361 iairgyglfa gpckvinakd vdfmyveliq rckqmfltqt dtgdyrvyqm psflqsvasv 421 llyldtvpev ytpvlehlvv mqidsfpqys pkmqlvccra ivkvflalaa kgpvlrncis 481 tvvhqgliri cskpvvlpkg pesesedhra sgevrtgkwk vptykdyvdl frhllssdqm 541 mdsiladeaf fsvnsssesl nhllydefvk svlkivekld ltleigtvge gengdeapgv 601 wmiptsdpaa nlhpakpkdf safinlvefc reilpekqae ffepwysfs yelilqstrl 661 plisgfykll sitvrnakki kyfegvspks lkhspedpek yscfalfvkf gkevavkmkq 721 ykdellasci tfilsiphni ieldvrayvp alqmafklgi sytplaevgi naleewsiyi 781 drhvmqpyyk dilpcldgyl ktsalsdetk nnwevsalsr aaqkgfnkvv lkhlkktknl 841 ssneaislee irirvvqmlg slggqinknl ltvtssdemm ksyvawdrek rlsfavpfre 901 mkpvifldvf lprvtelalt asdrqtkvaa cellhsmvmf mlgkatqmpe ggqgappmyq 961 lykrtfpvll rlacdvdqvt rqlyeplvmq lihwftnnkk fesqdtvsll eaildgivdp 1021 vdstlrdfcg rcireflkws ikqitpqqqe kspvntkslf krlyslalhp nafkrlgasl 1081 afnniyrefr eeeslveqfv fealviymes lalahadeks lgtiqqccda idhlcriiek 1141 khvslnkakk rrlprgfpps aslclldlvk wllahcgrpq tecrhksiel fykfvpllpg 1201 nrspnlwlkd vlkeegvsfl intfegggcg qpsgilaqpt llylrgpfsl qatlcwldll 1261 laalecyntf igertvgalq vlgteaqssl lkavaffles iamhdiiaae kcfgtgaagn 1321 rtspqegery nyskctvvvr imeftttlln tspegwkllk kdlcnthlmr vlvqtlcepa 1381 sigfnigdvq vmahlpdvcv nlmkalkmsp ykdilethlr ekitaqsiee lcavnlygpd 1441 agvdrsrlaa vvsackqlhr agllhnilps qstdlhhsvg tellslvykg iapgderqcl 1501 psldlsckql asgllelafa fgglcerlvs lllnpavlst aslgssqgsv ihfshgeyfy 1561 slfsetinte llknldlavl elmqssvdnt kmvsavlngm ldqsfreran qkhqglklat 1621 tilqhwkkcd swwakdsple tkmavlalla kilqidssvs fntshgsfpe vfttyislla 1681 dtkldlhlkg qavtllpfft sltggsleel rrvlegliva hfpmqsrefp pgtprfnnyv 1741 dcmkkfldal elsqspmlle lmtevlcreq qhvmeelfqs sfrriarrgs cvtqvglles 1801 vyemfrkddp rlsftrqsfv drslltllwh csldalreff stivvdaidv lksrftklne 1861 stfdtqitkk mgyykildvm ysrlpkddvh akeskinqvf hgscitegne ltktliklcy 1921 daftenmage nqllerrrly hcaayncais viccvfnelk fyqgflfsek peknllifen 1981 lidlkrrynf pvevevpmer kkkyieirke areaangdsd gpsymsslsy ladstlseem 2041 sqfdfstgvq sysyssqdpr patgrfrrre qrdptvhddv lelemdelnr hecmapltal 2101 vkhmhrslgp pageedsvpr dlpswmkflh gklgnpivpl nirlflaklv inteevfrpy 2161 akhwlspllq laasenngge gihymvveiv atilswtgla tptgvpkdev lanrllnflm 2221 khvfhpkrav frhnleiikt lvecwkdcls ipyrlifekf sgkdpnskdn svgiqllgiv 2281 mandlppydp qcgiqsseyf qalvnnmsfv rykevyaaaa evlglilryv merknilees 2341 lcelvakqlk qhqntmedkf ivclnkvtks fppladrfmn avffllpkfh gvlktlclev 2401 vlcrvegmte lyfqlkskdf vqvmrhrder qkvcldiiyk mmpklkpvel rellnpvvef 2461 vshpsttcre amynilmwih dnyrdpeset dndsqeifkl akdvliggli denpglqlii 2521 rnfwshetrl psntldrlla lnslyspkie vhflslatnf llemtsmspd ypnpmfehpl 2581 secefgeyti dsdwrfrstv ltpmfvetqa sqgtlqtrtq egslsarwpv agqiratqqq 2641 hdftltqtad grssfdwltg sstdplvdht spssdsllfa hkrserlqra plksvgpdfg 2701 kkrlqlpqde vdnkvkgaag rtdllrlrrr fmrdqeklsl myarkgvaeq krekeiksel

FIG. 11C

2761 kmkqdaqvvl yrsyrhgdlp diqikhssli tplqavaqrd piiakqlfss lfsgilkemd 2821 kfktlseknn itgkligdfn rflnttfsff ppfvscigdi scqhaallsi dpaavsagcl 2881 aslqqpvgir lleealirli paelpakrvr gkarlppdvl rwvelaklyr sigeydvlrg 2941 iftseigtkg itgsallaea rsdyseaakg ydealnkgdw vdgepteaek dfwelasldc 3001 ynhlaewksl eycstasids enppdlnkiw sepfygetyl pymirsklkl llggeadgsl 3061 ltfidkamhg elqkailelh ysgelsllyl lqddvdraky yiqngiqsfm qnyssidvll 3121 hqsrltklqs vqalteiqef isfiskqgnl ssqvplkrll ntwtnrypda kmdpmniwdd 3181 iitnrcffls kieekltplp ednsmnvdqd gdpsdrmevq eqeedissli rsckfsmkmk 3241 midsarkqnn fslamkllke lhkesktrdd wlvswvqsyc rlshcrsrsq gcseqvltvl 3301 ktvslldenn vssylxknil afrdqnillg ttyriianal ssepaclaei eedkarrile 3361 lsgsssedse kviaglygra fqhlseavga aeeeagppsw scgpaagvid aymtladfcd 3421 gqlrkeeena svtdsaelga ypalvvekml kalklnsnea rlkfprllgi ierypeetls 3481 1mtkeissvp cwqfiswish mvalldkdqa vavqhsveei tdnypqaivy pfiissesys 3541 fkdtstghkn kefvariksk ldqggviqdf inaldqlsnp ellfkdwsnd vraelaktpv 3601 nkkniekmye rmyaalgdpk apglgafrrk fiqtfgkefd khfgkggskl lrmklsdfnd 3661 itnmlllkmn kdskppgnlk ecspwmsdfk veflrnelei pgqydgrgkp lpeyhvriag 3721 fdervtvmas lrrpkriiir ghderehpfl vkggedlrqd qrveqlfqvm ngilaqdsac 3781 sqralqlrty svvpmtssdp rappceykdw ltkmsgkhdv gaymlmykga nrtetvtser 3841 kreskvpadl lkrafvrmst speaflalrs hfasshalic ishwilgigd rhlnnfmvam 3901 etggvigidf ghafgsatqf lpvpelmpfr ltrqfinlml pmketglmys imvhalrafr 3961 sdpglltntm dvfvkepsfd wknfeqkmlk kggswigein vaeknwyprq kicyakrkla 4021 ganpavitcd elllghekap afrdyvavar gskdhniraq epesglseet qvkcimdqat 4081 dpnilgrtwe gwepwm

FIG. 12A

LOCUS 130781 1014 aa 01-NOV-1997 DEFINITION POLY (ADP-RIBOSE) POLYMERASE (PARP) (ADPRT) (NAD(+)ADP-RIBOSYLTRANSFERASE) (POLY(ADP-RIBOSE) SYNTHETASE). ACCESSION 130781 PIDg130781 SWISS-PROT: locus PPOL_HUMAN, accession P09874 DBSOURCE class: standard. created: Mar 1, 1989. sequence updated: Dec 1, 1992. annotation updated: Nov 1, 1997. xrefs: gi: 510112, gi: 1017423, gi: 190166, gi: 190167, gi: 337423, gi: 337424, gi: 178151, gi: 178152, gi: 190266, gi: 190267, gi: 178188, gi: 178190, gi: 189533, gi: 189534, gi: 35286, gi: 825702, gi: 35288, gi: 189535, gi: 189536, gi: 88229, gi: 88227, gi: 627553, gi: 107162, gi: 107160, gi: 482956, gi: 420073, gi: 107158 xrefs (non-sequence databases): AARHUS/GHENT-2DPAGE 1620, MIM 173870, MIM 173871, PROSITE PS00347, PROSITE PS50064 TRANSFERASE; GLYCOSYLTRANSFERASE; NAD; DNA-KEYWORDS BINDING; NUCLEAR PROTEIN; ADP-RIBOSYLATION; ZINC-FINGER; ZINC. human. SOURCE ORGANISM Homo sapiens Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (residues 1 to 1014) AUTHORS Auer, B., Nagl, U., Herzog, H., Schneider, R. and Schweiger, M. Human nuclear NAD+ ADP-ribosyltransferase(polymerizing): TITLE organization of the gene JOURNAL DNA 8 (8), 575-580 (1989) MEDLINE 90091744 REMARK SEQUENCE FROM N.A. REFERENCE 2 (residues 1 to 1014) AUTHORS Uchida, K., Morita, T., Sato, T., Ogura, T., Yamashita, R., Noguchi,S., Suzuki, H., Nyunoya, H., Miwa, M. and Sugimura, T. Nucleotide sequence of a full-length cDNA for human fibroblast poly(ADP-ribose) polymerase

JOURNAL Biochem. Biophys. Res. Commun. 148 (2), 617-622 (1987) MEDLINE 88076933

REMARK SEQUENCE FROM N.A.

TISSUE=FIBROBLAST

FIG. 12B

1 maessdklyr veyaksgras ckkcsesipk dslrmaimvq spmfdgkvph wyhfscfwkv 61 ghsirhpdve vdgfselrwd dqqkvkktae aggvtgkgqd gigskaektl gdfaaeyaks						
0.1	dustrubase	vagiseirwa	dookvkktae	aggytgkggd	minekaektl	adfaaovaka
121	nrstckgcme	kiekggyrls	kkmydpekpa	lomidrwyhn	gcfvknreel	afronevesea
181	lkgfsllate	dkealkkglp	avkseakrka	devidovideva	kkkskkekdk	deklokalka
241	andliwnika	elkkycstnd	lkellifnka	acvagvaeva	drvadgmvfg	uskiekaika
301	glyfksdawy	ct adut aut k	TWEITITHING	dobpassair	divadgmvig	arrpceecsg
361	tesevestan	Dotooo	ChivKtqtpnr	Kewvtpkeir	eisylkklkv	kkqdrifppe
401	csasvaatpp	pscasapaav	nssasadkpl	snmkiltlgk	lsrnkdevka	mieklggklt
421	grankasici	stkkevekmn	kkmeevkean	irvvsedflq	dvsastkslq	elflahilsp
451	wgaevkaepv	evvaprgksg	aalskkskoo	vkeeginkse	krmkltlkaa	afrahahras
241	nsanviekgg	KVISatigly	divkgtnsvv	klalleddke	nrvwi frswa	ryatyjaenk
601	legmpskeda	iehfmklyee	ktonawhskn	ftkvnkkfvn	leidygqdee	aukkltumna
661	tksklpkpva	dlikmifdve	smkkamveve	idlakmolak	lskrqiqaay	ailannan
721	saassasail	dlsnrfvtli	nhdfamkknn	llanadanea	kvemldnlld	siisevaaav
781	aeggeekgai	dramable let a	phorgakkpp	TIMausvga	KAGUTAUTTA	ievayslirg
0/1	gaddaakupi	dvillex 1 ktd	ikvvarasee	aelirkyvkn	thatthnayd	levidifkie
841	regecdrykp	rkdruuttii	whgsrttnfa	gilsqglria	ppeapvtgym	fgkgiyfadm
901	vsksanycht	sqgapiglil	lgevalonmy	elkhashisk	lpkakhsyka	lakttnanea
961	nisldgvdvp	lgtgissgvn	dtsllyneyi	vydiagvnlk	vllklkfnfk	tslw